2

RAW SEQUENCE LISTING DATE: 10/14/2001 PATENT APPLICATION: US/09/770,102 TIME: 15:25:50

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10122001\I770102.raw

```
146 <213> ORGANISM: Unknown
    148 <220> FEATURE:
    149 <223> OTHER INFORMATION: O-GlcNAc site
    151 <220> FEATURE:
    152 <221> NAME/KEY: DOMAIN
    153 <222> LOCATION: (1)..(18)
    154 <223> OTHER INFORMATION: O-GlcNAc site
    157 <400> SEQUENCE: 7
    159 Asp Ser Ser Thr Asp Leu Thr Gln Thr Ser Ser Ser Gly Thr Val Thr
    160 1
    162 Leu Pro
    165 <210> SEQ ID NO: 8
    166 <211> LENGTH: 12
    167 <212> TYPE: PRT
    168 <213> ORGANISM: Unknown
    170 <220> FEATURE:
    171 <223> OTHER INFORMATION: O-GlcNAc site
     173 <220> FEATURE:
     174 <221> NAME/KEY: DOMAIN
    175 <222> LOCATION: (1)..(12)
    176 <223> OTHER INFORMATION: O-GlcNAc site
    179 <400> SEQUENCE: 8
    181 Met Ala Gly Gly Pro Ala Asp Thr Ser Asp Pro Leu
                                              1.0
    182 1
     184 <210> SEQ ID NO: 9
     185 <211> LENGTH: 13
     186 <212> TYPE: PRT
     187 <213> ORGANISM: Unknown
     189 <220> FEATURE:
     190 <223> OTHER INFORMATION: O-GlcNAc site
     192 <220> FEATURE:
     193 <221> NAME/KEY: DOMAIN
     194 <222> LOCATION: (1)..(13)
     195 <223> OTHER INFORMATION: O-GlcNAc site
     198 <400> SEQUENCE: 9
     200 Ala Gln Thr Ile Thr Ser Glu Thr Pro Ser Ser Thr Thr
                                              10
     201 1
     203 <210> SEQ ID NO: 10
     204 <211> LENGTH: 8
     205 <212> TYPE: PRT
     206 <213> ORGANISM: Unknown
     208 <220> FEATURE:
     209 <223> OTHER INFORMATION: Consensus sequence
     211 <220> FEATURE:
     212 <221> NAME/KEY: DOMAIN
     213 <222> LOCATION: (1)..(8)
     214 <223> OTHER INFORMATION: X at position 3 may be any amino acid
     217 <400> SEQUENCE: 10
W--> 219 Arg Arg Xaa Arg Arg Xaa/Ser Thr
```

What about Xaa at b?

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.